

Bioinformatics Studies on Evolutionary Patterns in Restriction Endonucleases

Tiratha Raj Singh^{1,2,*} and Kamal Raj Pardasani¹

¹Department of Mathematics, MANIT, Bhopal, India

²Department of Zoology, Faculty of life Sciences, Tel-Aviv University, Tel-Aviv, Israel.

Abstract

Restriction endonucleases represent one of the best studied examples of DNA binding proteins. Type II restriction endonucleases (REnases) recognize short sequences of foreign DNA and cleave the target on both strands with remarkable sequence specificity. Type II REnases are part of restriction modification (RM) systems. RM systems occur ubiquitously among Bacteria and Archaea. REnases are indispensable tools in molecular biology and biotechnology. They are important model system for specific protein-nucleic acid interactions and also serve as good example for investigating structural, functional and evolutionary relationships among various biomolecules. The interaction between REnases and their recognition sequences (RSs) plays crucial role in biochemical activities like catalytic site/metal binding, DNA repair and recombination etc. We study various patterns in REnases type II and analyze their structural, functional and evolutionary role. Based on our analysis, a computational protocol has been developed. Our studies support x-ray crystallographic studies, consequence for divergence and molecular evolution.

* Author for correspondence: trajsingh@rediffmail.com

² Present Address